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SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANTS: James M. Anderson
Christina M. Van Itallie
- (ii) TITLE OF INVENTION: Human Occludin, Its Uses
and Enhancement of Drug Absorption Using Occlu-
din Inhibitors
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Yale University Medical School
Section of Pulmonary and Critical Care Medicine
Department of Internal Medicine
 - (B) STREET: 333 Cedar Street, LCI 105
 - (C) CITY: New Haven
 - (D) STATE: Connecticut
 - (E) COUNTRY: United States of America
 - (F) ZIP CODE: 065220-8057
- (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: 3.5" 1.44 Mb diskette
 - (B) COMPUTER: IBM PC
 - (C) OPERATING SYSTEM: MS DOS
 - (D) SOFTWARE: Word Processing
- (vi) CURRENT APPLICATION DATA
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: June 25, 2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: U.S. 09/142,732
 - (B) FILING DATE: September 15, 1998
 - (C) CLASSIFICATION: 530-350.000
- (viii) ATTORNEY INFORMATION
 - (A) NAME: Mary M. Krinsky
 - (B) REGISTRATION NO.: 32423
 - (C) REFERENCE/DOCKET NUMBER: OCR-754.CIP
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE NUMBER: 203-773-9544
 - (B) TELEFAX NUMBER: 203-773-1183

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2312
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: cDNA

(v) FRAGMENT TYPE: complete sequence

(ix) FEATURE:

- (A) NAME/KEY: human occludin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

| | | | | | |
|------------|------------|------------|------------|------------|------|
| GCCTCTCTCC | ATCAGACACC | CCAAGGTTCC | ATCCGAAGCA | GGCGGAGCAC | 50 |
| CGAACGCACC | CCGGGGTGGT | CAGGGACCCC | CATCCGTGCT | GCCCCCTAGG | 100 |
| AGCCCGCGCC | TCTCCTCTGC | GCCCCGCCTC | TCGGGCCGCA | ACATCGCGCG | 150 |
| GTTCTTTTAA | CAGCGCGCTG | GCAGGGTGTG | GGAAGCAGGA | CCGCGTCCTC | 200 |
| CCGCCCCCTC | CCATCCGAGT | TTCAGGTGAA | TTGGTCACCG | AGGGAGGAGG | 250 |
| CCGACACACC | ACACCTACAC | TCCCGCGTCC | ACCTCTCCCT | CCCTGCTTCC | 300 |
| TCTTGCGCGA | GGCGGCAGGA | ACCGAGAGCC | AGGTCCAGAG | CGCCGAGGAG | 350 |
| CCGGTCTAGG | ACGCAGCAGA | TTGGTTTATC | TTGGAAGCTA | AAGGGCATTG | 400 |
| CTCATCCTGA | AGATCAGCTG | ACCATTGACA | ATCAGCCATG | TCATCCAGGC | 450 |
| CTCTTGAAAG | TCCACCTCCT | TACAGGCCTG | ATGAATTCAA | ACCGAATCAT | 500 |
| TATGCACCAA | GCAATGACAT | ATATGGTGGA | GAGATGCATG | TTCGACCAAT | 550 |
| GCTCTCTCAG | CCAGCCTACT | CTTTTTACCC | AGAAGATGAA | ATTCTTCACT | 600 |
| TCTACAAATG | GACCTCTCCT | CCAGGAGTGA | TTCGGATCCT | GTCTATGCTC | 650 |
| ATTATTGTGA | TGTGCATTGC | CATCTTTGCC | TGTGTGGCCT | CCACGCTTGC | 700 |
| CTGGGACAGA | GGCTATGGAA | CTTCCCTTTT | AGGAGGTAGT | GTAGGCTACC | 750 |
| CTTATGGAGG | AAGTGGCTTT | GGTAGCTACG | GAAGTGGCTA | TGGCTATGGC | 800 |
| TATGGTTATG | GCTATGGCTA | CGGAGGCTAT | ACAGACCCAA | GAGCAGCAAA | 850 |
| GGGCTTCATG | TTGGCCATGG | CTGCCTTTTG | TTTCATTGCC | GCGTTGGTGA | 900 |
| TCTTTGTTAC | CAGTGTTATA | AGATCTGAAA | TGTCCAGAAC | AAGAAGATAC | 950 |
| TACTTAAGTG | TGATAATAGT | GAGTGCTATC | CTGGGCATCA | TGGTGTTTAT | 1000 |
| TGCCACAATT | GTCTATATAA | TGGGAGTGAA | CCCAACTGCT | CAGTCTTCTG | 1050 |
| GATCTCTATA | TGGTTCACAA | ATATATGCCC | TCTGCAACCA | ATTTTATACA | 1100 |
| CCTGCAGCTA | CTGGACTCTA | CGTGGATCAG | TATTTGTATC | ACTACTGTGT | 1150 |
| TGTGGATCCC | CAGGAGGCCA | TTGCCATTGT | ACTGGGGTTC | ATGATTATTG | 1200 |

TGGCTTTTGC TTTAATAATT TTCTTTGCTG TGAAAACCTCG AAGAAAGATG 1250
 GACAGGTATG ACAAGTCCAA TATTTTGTGG GACAAGGAAC ACATTTATGA 1300
 TGAGCAGCCC CCCAATGTCG AGGAGTGGGT TAAAAATGTG TCTGCAGGCA 1350
 CACAGGACGT GCCTTCACCC CCATCTGACT ATGTGGAAAG AGTTGACAGT 1400
 CCCATGGCAT ACTCTTCCAA TGGCAAAGTG AATGACAAGC GGTTTTATCC 1450
 AGAGTCTTCC TATAAATCCA CGCCGGTTCC TGAAGTGGTT CAGGAGCTTC 1500
 CATTAACTTC GCCTGTGGAT GACTTCAGGC AGCCTCGTTA CAGCAGCGGT 1550
 GGTAACTTTG AGACACCTTC AAAAAGAGCA CCTGCAAAGG GAAGAGCAGG 1600
 AAGGTCAAAG AGAACAGAGC AAGATCACTA TGAGACAGAC TACACAACCTG 1650
 GCGGCGAGTC CTGTGATGAG CTGGAGGAGG ACTGGATCAG GGAATATCCA 1700
 CCTATCACTT CAGATCAACA AAGACAACCTG TACAAGAGGA ATTTTGACAC 1750
 TGGCCTACAG GAATACAAGA GCTTACAATC AGAACTTGAT GAGATCAATA 1800
 AAGAACTCTC CCGTTTGGAT AAAGAATTGG ATGACTATAG AGAAGAAAGT 1850
 GAAGAGTACA TGGCTGCTGC TGATGAATAC AATAGACTGA AGCAAGTGAA 1900
 GGGATCTGCA GATTACAAAA GTAAGAAGAA TCATTGCAAG CAGTTAAAGA 1950
 GCAAATTGTC ACACATCAAG AAGATGGTTG GAGACTATGA TAGACAGAAA 2000
 ACATAGAAGG CTGATGCCAA GTTGTTTGAG AAATTAAGTA TCTGACATCT 2050
 CTGCAATCTT CTCAGAAGGC AAATGACTTT GGACCATAAC CCCGGAAGCC 2100
 AAACCTCTGT GAGCATCACA AAGTTTTTGGG TTGCTTTAAC ATCATCAGTA 2150
 TTGAAGCATT TTATAAATCG CTTTTGATAA TCAACTGGGC TGAACAACCTC 2200
 CAATTAAGGA TTTTATGCTT TAAACATTGG TTCTTGTATT AAGAATGAAA 2250
 TACTGTTTGA GGTTTTTAAAG CCTTAAAGGA AGGTTCTGGT GTGAACTAAA 2300
 CTTTCACACC CC 2312

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: polypeptide

(v) FRAGMENT TYPE: complete sequence

(ix) FEATURE:

- (A) NAME/KEY: human occludin

[illegible]

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| Met | Ser | Ser | Arg | Pro 5 | Leu | Glu | Ser | Pro | Pro 10 | Pro | Tyr | Arg | Pro | Asp 15 |
| Glu | Phe | Lys | Pro | Asn 20 | His | Tyr | Ala | Pro | Ser 25 | Asn | Asp | Ile | Tyr | Gly 30 |
| Gly | Glu | Met | His | Val 35 | Arg | Pro | Met | Leu | Ser 40 | Gln | Pro | Ala | Tyr | Ser 45 |
| Phe | Tyr | Pro | Glu | Asp 50 | Glu | Ile | Leu | His | Phe 55 | Tyr | Lys | Trp | Thr | Ser 60 |
| Pro | Pro | Gly | Val | Ile 65 | Arg | Ile | Leu | Ser | Met 70 | Leu | Ile | Ile | Val | Met 75 |
| Cys | Ile | Ala | Ile | Phe 80 | Ala | Cys | Val | Ala | Ser 85 | Thr | Leu | Ala | Trp | Asp 90 |
| Arg | Gly | Tyr | Gly | Thr 95 | Ser | Leu | Leu | Gly | Gly 100 | Ser | Val | Gly | Tyr | Pro 105 |
| Tyr | Gly | Gly | Ser | Gly 110 | Phe | Gly | Ser | Tyr | Gly 115 | Ser | Gly | Tyr | Gly | Tyr 120 |
| Gly | Tyr | Gly | Tyr | Gly 125 | Tyr | Gly | Tyr | Gly | Gly 130 | Tyr | Thr | Asp | Pro | Arg 135 |
| Ala | Ala | Lys | Gly | Phe 140 | Met | Leu | Ala | Met | Ala 145 | Ala | Phe | Cys | Phe | Ile 150 |
| Ala | Ala | Leu | Val | Ile 155 | Phe | Val | Thr | Ser | Val 160 | Ile | Arg | Ser | Glu | Met 165 |
| Ser | Arg | Thr | Arg | Arg 170 | Tyr | Tyr | Leu | Ser | Val 175 | Ile | Ile | Val | Ser | Ala 180 |
| Ile | Leu | Gly | Ile | Met 185 | Val | Phe | Ile | Ala | Thr 190 | Ile | Val | Tyr | Ile | Met 195 |
| Gly | Val | Asn | Pro | Thr 200 | Ala | Gln | Ser | Ser | Gly 205 | Ser | Leu | Tyr | Gly | Ser 210 |
| Gln | Ile | Tyr | Ala | Leu 215 | Cys | Asn | Gln | Phe | Tyr 220 | Thr | Pro | Ala | Ala | Thr 225 |
| Gly | Leu | Tyr | Val | Asp 230 | Gln | Tyr | Leu | Tyr | His 235 | Tyr | Cys | Val | Val | Asp 240 |
| Pro | Gln | Glu | Ala | Ile 245 | Ala | Ile | Val | Leu | Gly 250 | Phe | Met | Ile | Ile | Val 255 |

Figure 1 is a schematic representation of the experimental design. It shows a flow from 'Study 1' to 'Study 2'. Study 1 involves 'Pretest' and 'Main Study'. Study 2 involves 'Pretest' and 'Main Study'. The 'Main Study' in both studies involves 'Participants' and 'Conditions'. The 'Conditions' are 'Control' and 'Intervention'. The 'Intervention' is 'Cognitive Behavioral Therapy (CBT)'. The 'Control' is 'Waitlist Control'. The 'Participants' are 'College Students'. The 'Conditions' are 'Control' and 'Intervention'. The 'Intervention' is 'Cognitive Behavioral Therapy (CBT)'. The 'Control' is 'Waitlist Control'. The 'Participants' are 'College Students'.

Cys Ser Tyr Gly Ser Gly Tyr Gly Tyr Gly Tyr Gly Tyr Gly Tyr
5 10 15

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Gly Tyr Gly Gly Tyr Thr Asp Pro Arg
20

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: peptide

(v) FRAGMENT TYPE: synthetic peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: construct used in experiments

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | His | Tyr | Ala | Pro | Ser | Asn | Asp | Ile | Tyr | Gly | Gly | Glu | Met | Val |
| | | | | 5 | | | | | 10 | | | | | 15 |
| His | Arg | Pro | Met | Leu | | | | | | | | | | |
| | | | | 20 | | | | | | | | | | |

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: peptide

(v) FRAGMENT TYPE: synthetic peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: construct used in experiments

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

| | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Gln | Gln | Val | Tyr | Arg | Lys | Asp | Pro | Cys |
| | | | | 5 | | | | | 10 | |